Editorial

Human Biology of Migration

How does migration influence and shape human biology? This was the central question posed to the participants of the 57th SSHB Symposium held in December 2016 at the Aarhus Institute of Advanced Studies at the University of Aarhus in Denmark. This special issue of the *Annals of Human Biology* contains papers by some of those participants and several specially selected papers that help to reflect the themes and questions explored during the meeting. The papers draw from methods and approaches across the spectrum of human biology and reflect the complex and interlinked processes that not only influence human migration, but also the signals and patterns it leaves in our biological make-up. In this introduction we give a broad overview of the arguments set out in those papers. We also unpack and discuss the main ideas underlying assumptions about what migration is, how it interacts with our biology, and what this process looks like. We end by exploring how migration across time and space has shaped modern human biology and continues to influence our daily lives.

Migration at its simplest is permanent or semi-permanent movement of people to a new location. It may be permanent, temporary, recurrent or seasonal and can take place in a single generation or across several. Underlying this simple concept is a complex series of processes that interact to influence multiple levels of human biology. Migration has a deep time frame in human development and is something of a common practice by our genus (Maslin et al. 2014; Houldcroft and Underdown 2016). Hominin dispersal within Africa was well established at least 3 million years ago with the dispersal of Australopithecus species from East Africa to Southern Africa (Clarke 2008). Subsequently, the trend started by *Homo erectus* around 1.8 MYA was the first of series of migration events that saw *Homo antecessor* colonise the Atapeurcan mountains in southern Spain around 1.2 MYA and *Homo heidelbergensis* extend its range from Africa to southern Britain and the Mediterranean (Lopez, van Dorp, and Hellenthal 2016; Mounier and Lahr 2016; Ferring et al. 2011). Similarly, the discovery of *Homo floresiensis* and the Denisovans reveal a complex mosaic movement and colonisation by the genus Homo during the Pleistocene (Brown et al. 2004). While it is arguable that this movement and of early human species was more akin to dispersal, the impact of human global colonisation that began around 100,000 years ago is not (Lopez, van Dorp, and Hellenthal 2016). The unparalleled expansion of the human species, in terms of both numbers and range, has created a number of unique challenges to human biology. The impact of human movement can leave a widely diverse range of biological signal ranging from eco-morphological adaption to climate, adaptive changes, genetic markers and patterns of disease resistance or susceptibility. This special issue explores patterns of past and present migration on human biology and ends with an eye to what we might expect in future.

Using germs and genetics to uncover past migration events

The signature left in genomic records provides a window into the co-evolutionary arms race between humans and pathogens. We know for example that Neanderthals and Denisovans were hunter-gatherers adapted to a Eurasian rather than African infectious disease package. Genomes also provide clues to past environments and the evolutionary pressures that shaped our physiology and behaviour in complex, dynamic ways. Research from the fields of molecular biology and ecology illustrate an increasingly complex relationship between our diet, (gut) microbes, behaviour and

disease (Mayer et al. 2014). For example, a shift towards a Neolithic diet and simple carbohydrates encouraged humans who outcompeted microbes for the new substrates thereby obtaining more energy from their diets, a shift that is visible in modern population genetics (Walter and Ley 2011). In light of recent developments in genomics, **Houldcroft and colleagues** (this issue) take up the baton and explore the traces left by pathogens on the archaeological record. They examine three pathogens. First, the interaction between colonialism, railway networks and the spread of HIV; secondly, the relationship between the trans-Atlantic slave trade, fresh-water fishing and the gut parasite *Schistosoma mansoni*; and finally the hints of hominin migration and human herpes simplex virus 2.

The challenge of unravelling the history of smaller-scale migrations in relatively narrow geographic areas using mitochondrial DNA (mtDNA) diversity is tackled by **Davidovic and colleagues** (this issue) on the basis of Slavic populations. Existing molecular evidence shows that Slavs are the most prevalent ethno linguistic group in Europe and stratified into three language groups (West-, East- and South Slavs), which are well distinguished genetically and geographically. Whereas West Slavs display a genetic affinity to German populations, Russians and South Slavs are genetically similar to Finno-Ugric populations from North-Eastern Europe and non-Slavic populations from the Balkan Peninsula. Given its role as a corridor between Europe and the Near East and also as a source for the post-glacial re-population of Europe, the Balkan Peninsula in particular is important in the evolutionary history of Europeans. Due to the turbulent demographic history of Slavs, especially after medieval expansion which sees the appearance of Huns, Avars, Magyars and Bulgars, questions remain about the female specific aspects of the history of South Slavs. Since the existing studies using mtDNA have low data resolution, Davidovic et al. analyse the complete mitochondrial genomes (mitogenomes) of 46 predominantly Serbian individuals and compare these to nearly 4000 complete mitogenomes of modern and ancient Western Eurasians.

In similar vein, but instead using Y chromosome diversity, **Babíc and colleagues** (this issue) unravel migration patterns in Tuzla Canton, the most populated region in Bosnia and Herzegovina. Existing archaeological evidence in the region implies that the area has been continuously populated for over 6000 years, which makes it one of the oldest sustained settlements in the region and has led to a high diversity in local populations. This makes it a prime candidate for insights into past demographic events which Babíc et al. explore by analysing 23 Y-chromosomal short tandem repeat (Y-STRY) in 100 unrelated, healthy adult males living in Tuzla Canton. Their aim is to compare Tuzla Canton populations to Bosnian and Herzegovinian data as a whole and also with local, neighbouring populations and other European populations.

The human biology of recent and present-day migrations

Arguably one of the biggest challenges in migration research is unravelling the multitude of complex interactions that leave a signature of migration, be it in terms of genetics, phenotype or linguistics for example, and determining causal and directional effects on human biology. To address this challenge **Mascie-Taylor** and **Krzyżanowska** (this issue) do a comprehensive review on how migration impacts variation in human biological traits. Starting with the early history and use of anthropometric indices, they review data from studies comparing sedente and migrant populations conducted across the globe since the beginning of the 20th Century. In addition to outlining key trends, processes and patterns in different populations, they also examine more subtle aspects, such

as comparing the level of social mobility with geographical (regional) migration. For example, in a British sample social mobility and geographical migration are not independent: socially non-mobile fathers and sons were more likely to be geographical non-migrants; conversely upwardly socially mobile fathers and sons are more likely to be regional migrants and are, on average, taller and had a lower BMI than non mobile fathers and sons. This paper also examines migration and mobility in relation to health, disease and nutrition. Mascie-Taylor and Krzyżanowska trace their way through huge historical populations shifts, precipitated by the Black Death in Europe and the Middle East, through to the devastating effects of measles epidemics in South America, and to the role migration has played in outbreaks of typhus, cholera and most recently HIV transmission. Contrary to popular perception, which often lays epidemics at the foot of migrant populations, they also draw attention to data illustrating that in some cases migrants are in better health and themselves at risk of disease from endemic populations. Finally, they consider the complex intersection where biology and culture meet, tracing the effects of migration on hypertension and cancer risk, blood group frequencies, metabolism, mental health and food and nutrition. The result is a comprehensive summary for anyone looking to gain an overview of the field.

With the aforementioned large-scale, global review as platform, we now move to a series of papers that illustrate the nuances of migration and migrants on a smaller, local scale. Migrants have a complex effect on the communities they enter and vice versa. One of the challenges of measuring the impact on either group is the fact that individual responses are influenced by a number of personal, socio-economic and cultural factors. Furthermore, not all migrants respond to the stress of migration in the same way and by virtue of the ever-present state of flux in communities receiving migrants or witnessing outward migration, assessing the changing cultural dynamics and impact on human biology is never straightforward. Nevertheless, two of our papers tackle this issue from a dietary perspective. Comparing two communities in Guatemala **McKerracher and colleagues** (this issue) focus their attention on testing evolutionary hypotheses that attempt to explain fertility increases in indigenous populations undergoing economic transitions. The first is the "energy access" hypothesis which assumes that fertility increases is associated with increased access to energy dense foods, increases in sedentism and the introduction of labour saving technology (Snopkowski and Kaplan 2014; Sear et al. 2016). The second is the "live fast-die young" hypothesis, which assumes that the emergence of markers of increasing fertility is driven by poor conditions (Charnov and Berrigan 2005; Walker et al. 2006). Using interview, biomolecular and anthropometric data from Maya women, McKerracher et al. assess fertility markers between two villages and between pre- and post-immigration periods. Specifically, they hypothesise that Maya women who interact more extensively with international migrants are exposed to higher levels of socioeconomic inequality and changes in diet and will show corresponding biologically meaningful changes in fertility. Similarly, **Osei-Kwasi and colleagues** examine the extent and consequences of dietary acculturation in adults of Ghanian ancestry living in greater Manchester, UK. Using demographic data and interviews they uncover three distinct dietary practices that differ in terms of meal formats, structure, preparation and food purchasing behaviours. Given the complex nature of dietary acculturation in these populations, this study has strong implications for practitioners seeking to implement dietary practice interventions among migrant populations.

The effect of relatively recent migrations on the genetic composition of different ethnic groups in China is covered in the following two papers. The first, by **Li and colleagues** (this issue) investigates the migration of Koreans who came to China in the late 19th and early 20th centuries and established

themselves as a major population group numbering nearly 2 million today. Tracking mtDNA control regions in nearly 300 Yanbian Korean individuals living in southeast China, they demonstrate that the Yanbian Korean population is an endogamous Northeast Asian group. The second paper by **Chen and colleagues** (this issue) uses polymorphic STR loci from nearly 200 unrelated, individuals from the Li ethnic group in Hainan Island, in the South China Sea. They seek to establish which populations the Li have the closest relationships with, where they came from, and whether the genetic data confirms the existing historical Dynasty records.

What the human biology of past and present migrations can tell us about managing future migrations

Given the current global (political) climate it was little surprise that the 57th Symposium on the Human Biology of Migration involved sobering data from the UN Refugee Agency. With an unprecedented 22.5 million refugees worldwide, over half of who are under the age of 18, the effects of mass migration are clearly evident (UNHCR 2016). Less so is how migrants and host nations negotiate these vast population shifts. To that end **Hvas and Wejse** (this issue) systematically review the type and extent of health assessments of refugees after resettlement. Combining data from 47 studies from North America, Australia, New Zealand and Europe they discuss not only who is offered health assessment, but also which diseases are most frequently screened, which were neglected and provide suggestions on how to address shortcomings. Finally, **Athanasiadis** (this issue) explores why it is important to steer clear of biological or historical data on migration when it comes to immigration rhetoric or policies. Using evidence from the genetic structure of a Danish population he illustrates the challenges created by the narrow time periods that many human population genetic studies rely on.

Conclusion

The impact of migration on human biology is profound. From the shadows cast by human dispersals in deep time to the modern health implications posed by movement of large numbers of people the subject remains at the top of the agenda of researchers across the discipline of human biology and beyond. The deeply interdisciplinary nature of this symposium reflects the complexities of trying to unpick how migration interacts with our biology from the genetic and cellular level through to socio-political implications of large-scale movement in the 21st Century.

The 57th SSHB Symposium successfully brought together together researchers and practitioners from across a wide range of disciplines and research methods, but who ultimately were all focussed on the interplay between migration and biology. This special issue of the *Annals of Human Biology* is intended to mirror the interdisciplinary nature of the meeting and hopefully to showcase new ideas, thinking and research agenda that can cut across traditional subject divisions and help to elucidate the role of migration in shaping human biology.

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